

Figure 1. Single-crossover recombination.

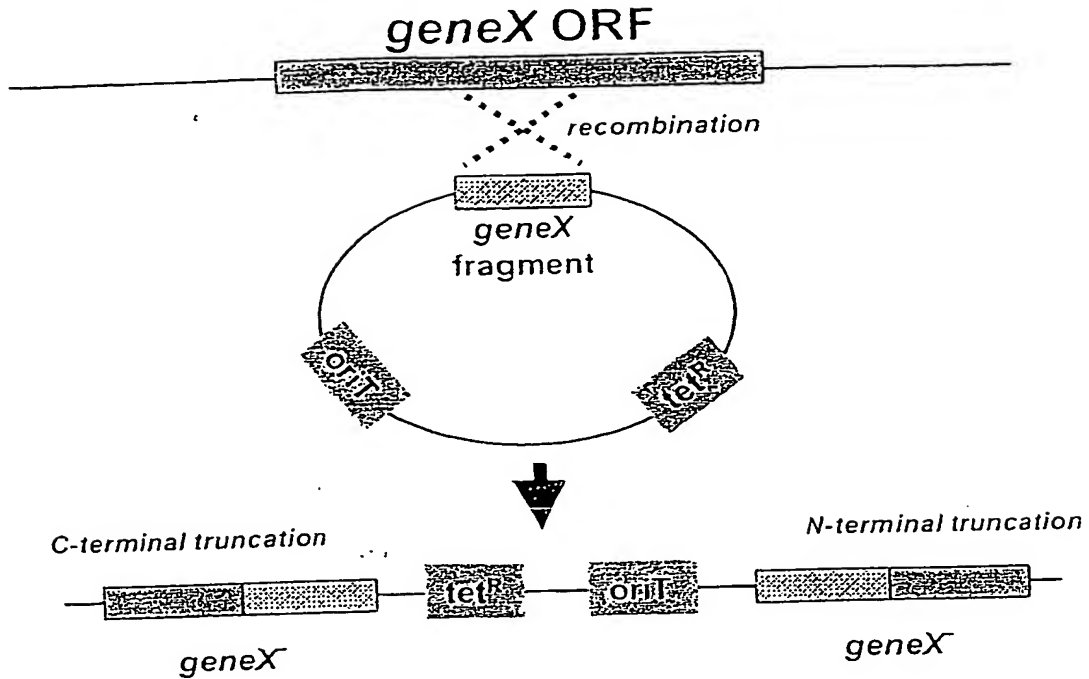
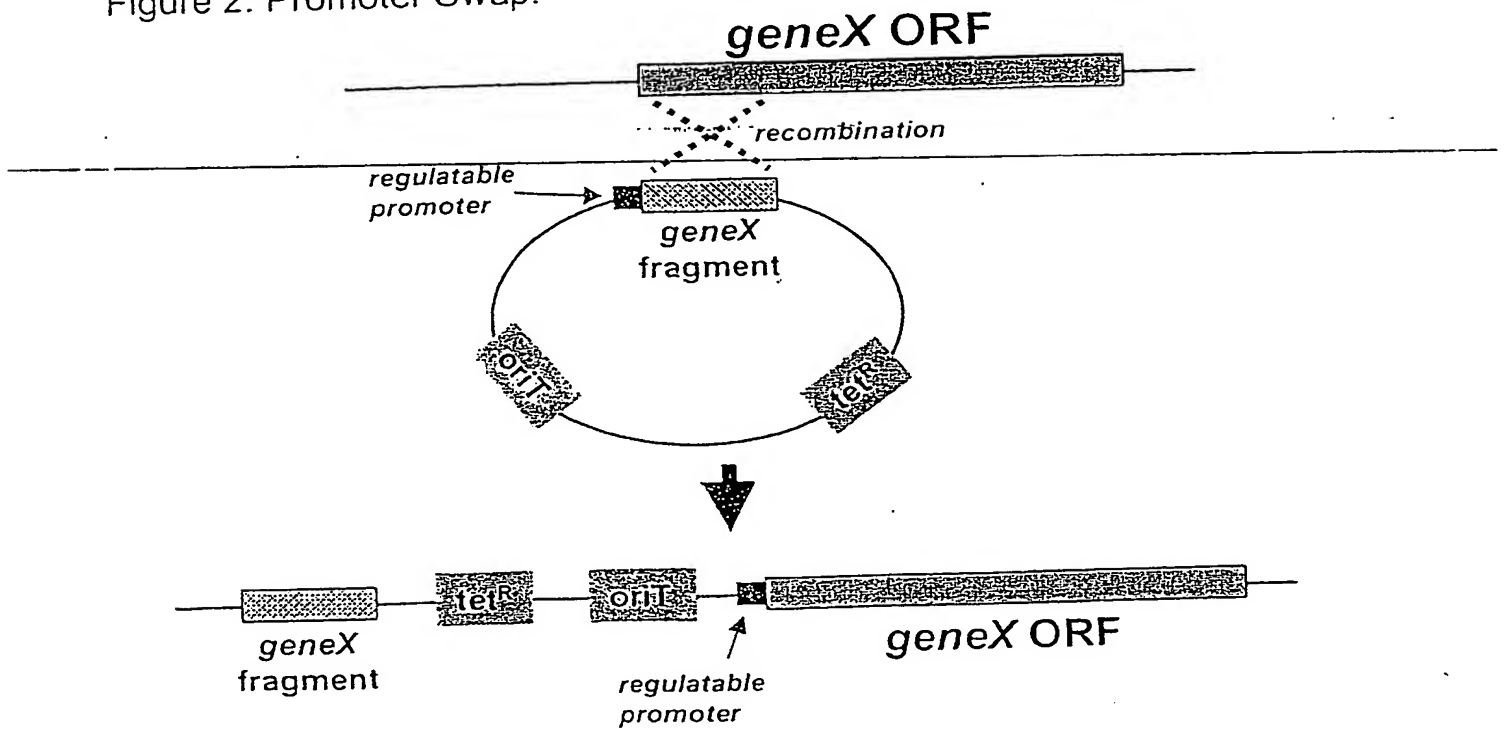


Figure 2. Promoter Swap.



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pMOD

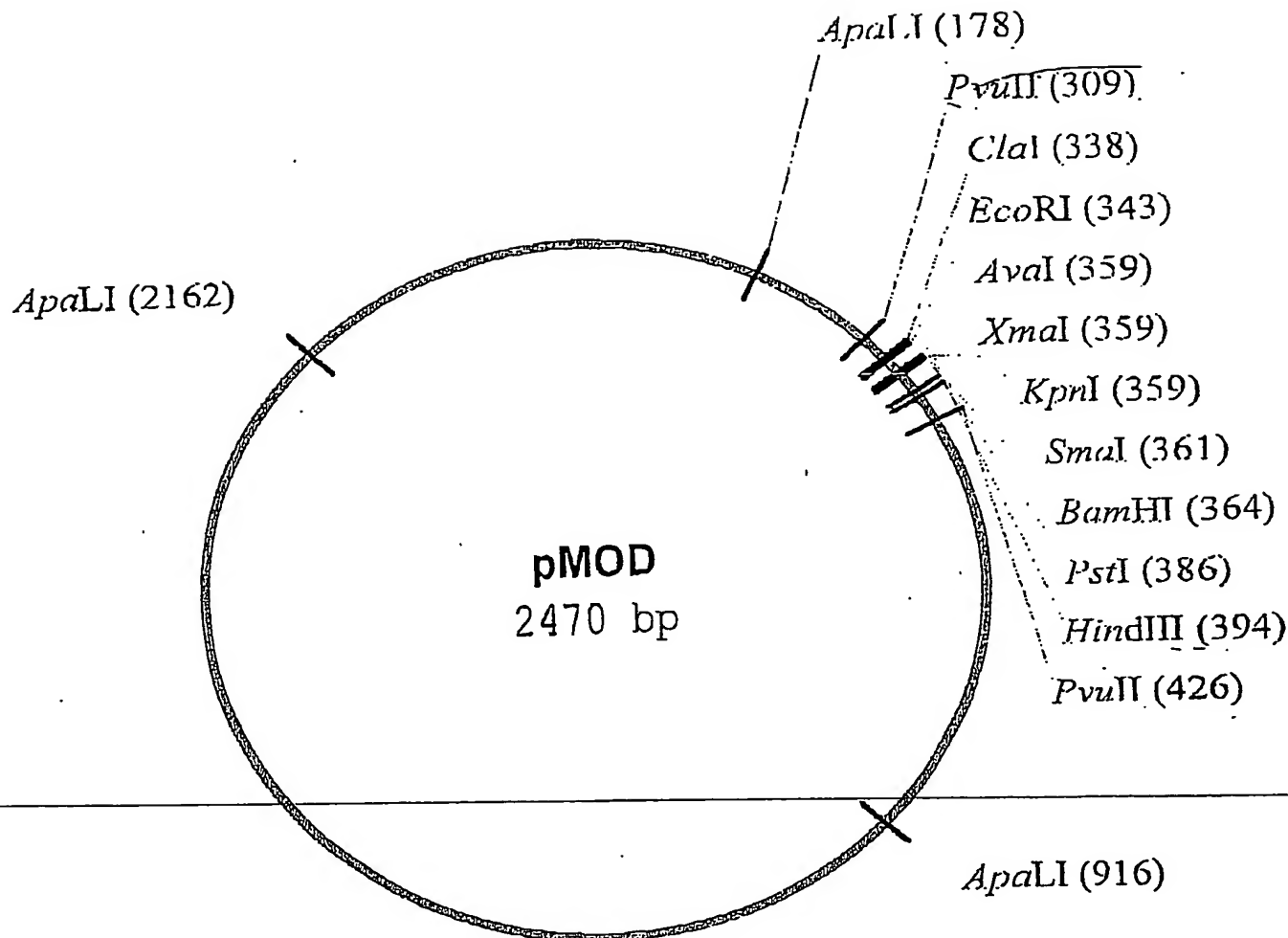


FIGURE 3

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pMOD (Erm-1)

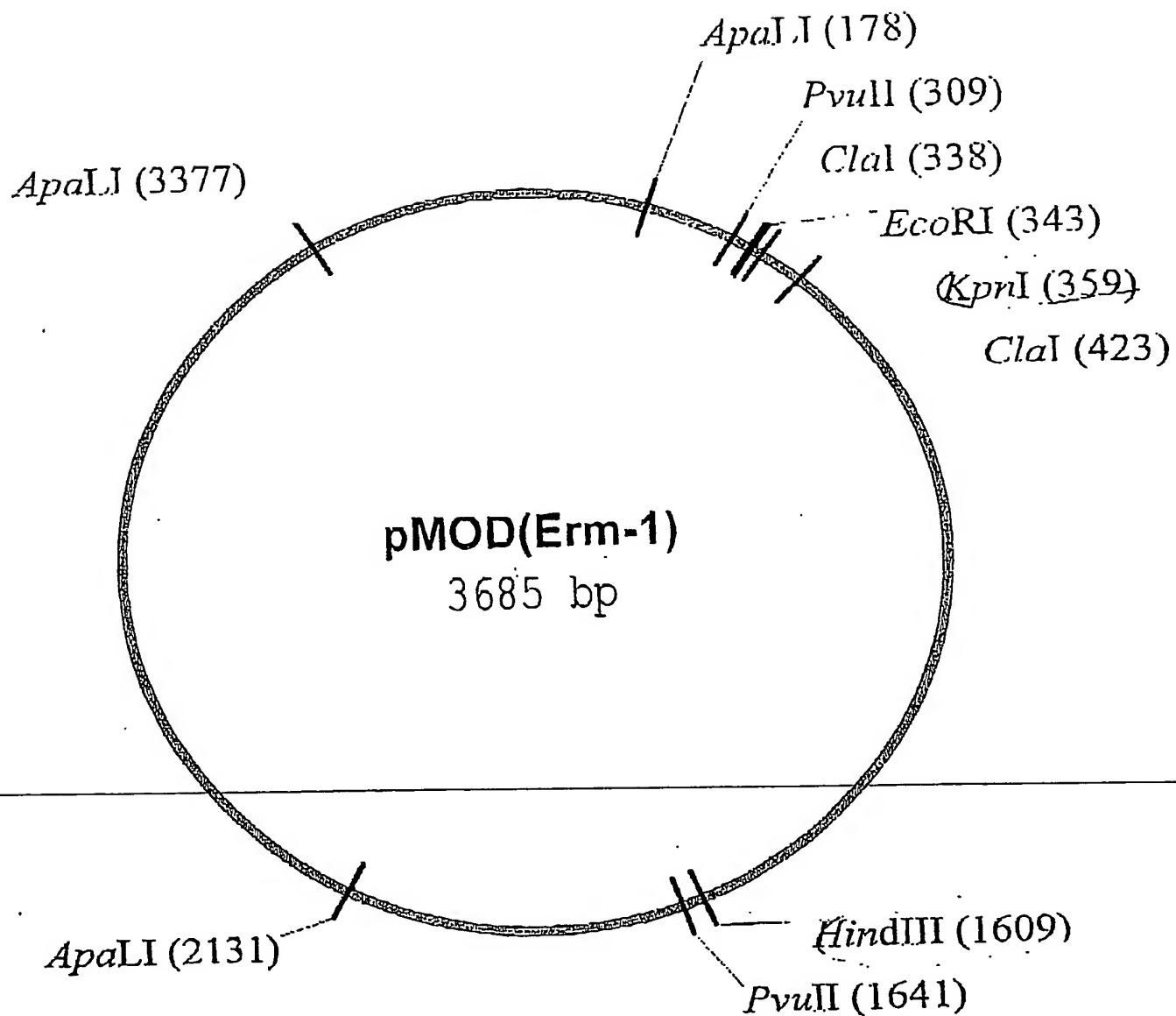
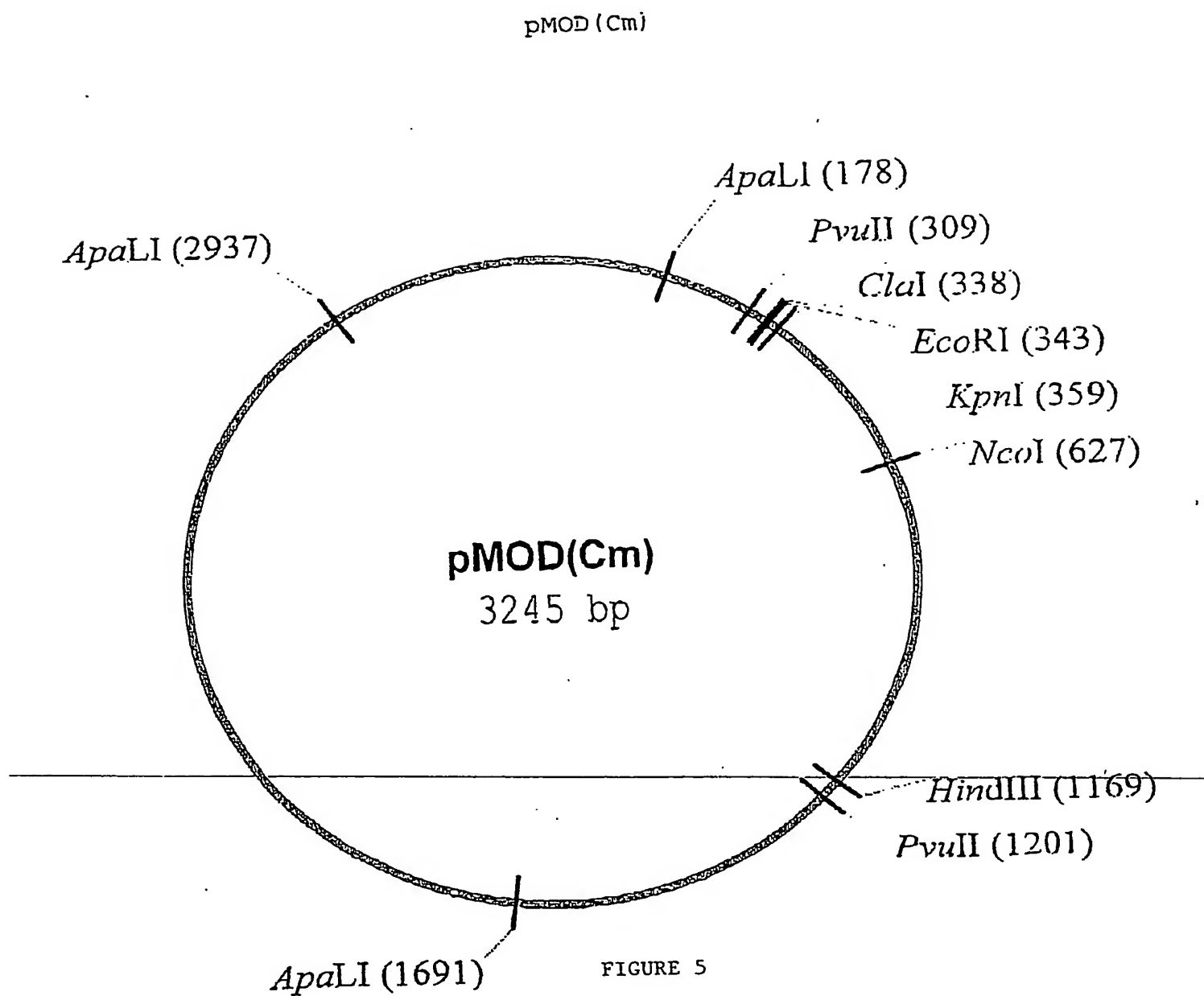


FIGURE 4



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FIGURE 6

pMOD

1 TCGCGCGTTT CGGTGATGAC GGTGAAACC TGTGACACAT GCAGCTCCCG
 AGUGCGCAAA GCCACTACTG CCACTTTTGG AGACTGTGTA CCGCCACCGC
 51 GAGACGGTCA CAGCTTCTCT GTAAGGGAT GUGUGGAGCA GACAAGCGCG
 CTCTGCCAGT GTCGAACACA CATTGCGCTA CGCCCTTGGT CTGTTGGGGC
 101 TCAGGGCGCG TCAGCGGGTG TTGGCGGGTG TCGGCGCTGG CTTAAGTATG
 AGTCCCGCGC AGTCGCCCCAC AACCGCCAC AGCCCCGACC GAATTGATAC
 ApaLI
 151 CCGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATCGG GTGTGAAATA
 GCCGTAGTCT CGTCTACAT GACTCTCAGG TGGTATACCG CACACTTTAT
 201 CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGCCGCC ATTGGCCATT
 GCGGTGTCTA CGCATTCCTC TTTTATGGCG TAGTCCCGCG TAAGCGGTAA
 251 CAGCCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTGGCTAT
 GTCGACGCG TTGACAACCC TTCCCGCTAG CAGCGCCCGG AGAAGCGATA
 EcoRI
 301 TACGCGAGCT GTCTCTTATA CACATCTCPA CCATCATCGA TCAATTCGAG
 ATGCGGTCTGA CAGAGAAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
 KpnI BamHI
 351 CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTCCAGGCAT GCAAGCTTCA
 GAGCCATGGG CCGCTAGGAG ATCTCAGCTG CACGTCCGTA CGTTCGAAGT
 SmaI XmaI Aval
 401 GGGTTGAGAT CTGTATAAGA GACAGCTGCA TTAATGAATC GCGCAACGCG
 CCGAACTCTA CACATATTCT CTGTGACGT AATTACTTAG CCGGTTGCGC
 451 CCGGGAGAGG CGGTTTGGCT ATTGCCCCCT CTTCGGCTTC CTCGCTCACT
 GCGGCTCTCC GCCAAACGCA TACCCCGCCA GAAGCGGAAG GAGCGACTCA
 501 GACTCGCTGC GCTCGGTCTG TCGGCTGCGG CGAGUGGTAT CAGCTCACTC
 CTGAGCGACG CGAGCCAGCA AGCCGACGCC GCTCGCCATA GTCEAGTGAG
 551 AAAGGCGGTA ATACGGTTAT CCACAGAATC AGGGGATAAC GCAGGAAAGA
 TTTCCGCCAT TATGCCAATA GGTGTCTTAG TCCCTATTG CGTCCTTTCT
 601 ACATGTGAGC AAAAGGCCAG CAAAGGCCA GGAACCGTAA AAAGGCCGCG
 TGTACACTCG TTTTCCGGTC GTTTTCCGGT CTTGGCATT TTTCCGGCGC
 651 TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCGACGAGC ATCACAAAA
 AACGACCGCA AAAAGGTATC CGAGGCGGGG GGAAGTCTCG TAGTGTTTTT
 701 TCGACGCTCA AGTCAGAGGT GGCGAAACCC GACAGGACTA TAAAGATACC
 AGCTGCGAGT TCAGTCTCCA CCGCTTTGGG CTGTCTGAT ATTTCTATCC
 751 AGGCGTTTCC CCGTGAAGC TCCCTCGTGC GCTCTCTGT TCCGACCTTG
 TCCGCAAAGG GGGACCTTCG AGGGAGCAGC CGAGAGGACA AGGCTGGGAC
 801 CCGCTTACCG GATACCTGTC CGCCTTTCTC CTTCCGGGAA GCGTGGCGCT
 GCGGAATGGC CTATGCACAG GCGGAAGAG GGAAGCCCTT CGCACCGGCA
 851 TTCTCATAGC TCACGCTGTA GGTATCTCAG TTCGGTGTAG GTCGTTCCCT
 AAGAGTATCG AGTGGGACAT CCATAGAGTC AAGCCACATC CAGCAAGCGA
 ApaLI
 901 CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA CCGCTGCGCC
 GGTTCGACCC GACACACGTG CTTGGGGCCC AGTCGGGCT GGCGACGCGG

pMOD

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951  TTATCCGGTA ACTATCGTCT TGAGTCCGAC CCGCTAGAGC AGGACTTATC
    AATAGGCCAT TGATAGCAGA ACTCAGGTTG GGCCATTCTG TGCTGAATAG
1001  GCCACTGGCA GCACCCACTG GTAACAGGAT TACCAGAGCG AGGTATGTAC
    CGCTGACCGT CGTCGGTGAC CATTTGCTTA ATCGTCTCGC TCCATACATC
1051  GCGGTGCTAC ACAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA
    CGCCACGATG TCTCAAGAAC TTCACCACCG CATTGATGCC GATGTGATCT
1101  AGGACAGTAT TTGGTATCTG CGTCTGCTG AAGCCAGTTA CCTTCCCAAA
    TCCTGTGATA AACCATAGAC GCGAGACGAC TTCGGTCAAT GGAAGCCTTT
1151  AAGAGTTCTG AGCTCTTGAT CCGGCAACA AACCAACGCT GGTAGCGCTG
    TTCTCAACCA TCGAGAATA GCGCGTTTGT TTGCTGGCGA CCATCGCCAC
1201  GTTTTTTTGT TTGCAAGCAG CAGATTACGC CCAGAAAAAA AGGATCTCAA
    CAAAAAACA AACGTTGCTC GTCTAATGCG CGTCTTTTTT TCCTAGAGTT
1251  GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA
    CTCTAGGAA ACTAGAAAAG ATGCCCCAGA CTGCGAGTCA CTTTGCTTTT
1301  CTCAGGTTAA GGGATTTTCC TCATGAGATT ATCAAAAGG ATCTTCACCT
    GAGTGCAATT CCTAAAACC AGTACTCTAA TAGTTTTTC TAGAAGTGG
1351  AGATCCTTTT AAATTAAAA TGAAGTTTAA AATCAATCTA AAGTATATAT
    TCTAGGAAAA TTAAATTTT ACTTCAAAAT TTAGTTAGAT TTCATATATA
1401  GAGTAAACTT GGTCTGACAG TTACCAATGC TTAATCAGTG AGGCACCTAT
    CTCATTTCAA CCAGACTGTC AATGGTTACG AATTAGTAC TCCTGGGATA
1451  CTCAGCGATC TGCTATTTTC GTTCATCCAT AGTTGGCTGA CTCCCCCTCG
    GAGTCGCTAG ACAGATAAAG CAAGTAGGTA TCAACGGACT GAGGGCCAGC
1501  TGTAGATAAC TACGATACGG GAGGGCTTAC CATCTGGCCC CAGTGTCTGA
    ACATCTATTG ATGCTATGCC CTCCCGAATG GTAGACGGG GTCACGACGT
1551  ATGATACCGC GAGACCCACG CTCACCGGCT CCAGATTTAT CAGCAATAAA
    TACTATGGCG CTCTCGGTGC GAGTGGCCCA GGTCTAAATA GTCGTTATTT
1601  CCAGCCAGCC GGAAGGGCCG AGCGCAGAAG TGGTCTTCCA ACTTTATCCG
    GGTGCGTGG CCTTCCCGGC TCGGCTCTTC ACCAGGACGT TCATATAGGC
1651  CCTCCATCCA GTCTATTAAT TGTTGCCCGG AAGCTAGAGT AAGTAGTTCC
    GGACCTAGGT CAGATAATTA ACAACGGCCC TTCGATCTCA TTCATCAAGC
1701  CCAGTTAATA GTTTGCGCAA CGTTGTGCCC ATTGCTACAG CCATCGTGGT
    GGTCAATTAT CAAACGCGT GCAACAACGG TAACGATGTC CGTAGCACCA
1751  GTCACGCTCG TCGTTTGGTA TGGCTTCATT CAGCTCCGGT TCCCAACGAT
    CAGTCCGAGC AGCAAACCAT ACCGAAGTAA GTGAGGCCA AGGGTTGCTA
1801  CAAGGCGAGT TACATGATCC CCCATGTTCT GCAAAAAACC GGTAGCTCC
    GTTCCGCTCA ATGTAAGAGG GGGTACAACA CGTTTTTTCG CCAATCGAGG
1851  TTCGGTCTTC CGATCGTTGT CAGAAGTAAG TTGGCCGCAC TGTATCACT
    AAGCCAGGAG GCTAGCAACA GTCTTCATTC AACCGCGCTC ACAATAGTGA
1901  CATGETTATG GCAGCACTGC ATAATTCTCT TACTGTCTAG CCATCCGTAA
    GTACCAATAC CGTCGTGACG TATTAAGAGA ATGACAGTAC GGTAGGCATT
1951  GATGCTTTTC TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG
    CTACGAAAAG AACTGACCA CTCATGAGT CGTTCAGTAA GACTCTTATC
2001  TGTATCGGCG GACCGAGTTC CTCATTGCCC GCGTCAATAC GGGATAATAC
    ACATACGCCC CTGGCTCAAC CAGAACGGGC CGCAGTTATG CCTATTATG
2051  CGCGCCACAT AGCAGAAGTT TAAAGTGCT CATCATTTGA AACGTTCTT
    GCGCGGTGTA TCGTCTTGAA ATTTTCACGA GTAGTAACCT TTTGCAAGAA
2101  CGGCGCGAAA ACTCTCAAGG ATCTTACCGC TGTGAGATC CAGTTCGATG
    GCGCGCTTT TGAGAGTTCC TAGAATGGCG ACAACTCTAG GTCAAGCTAC

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PMOD

ApalI
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|      |             |            |            |            |             |
|------|-------------|------------|------------|------------|-------------|
| 2151 | TPACCCACTC  | GTGCACCCAA | CTGATCTTCA | GCATCTTTTA | CTTTCACCCAC |
|      | ATTGGGGTGAG | CAUGTGGGTT | GACTAGAAAT | CGTAGAAAT  | GAAAGTGGTC  |
| 2201 | CGTTTTCTGCC | TGAGCAAAAA | CAGCAAGGCA | AAATGCCGCA | AAAAAGGGAA  |
|      | GCAAGAGCCC  | ACTCGTTTTT | GTCCTTCCGT | TTTACGGCGT | TTTTTCCCTT  |
| 2251 | TAAGGGGCGAC | ACGGAAATGT | TGAATACTCA | TACTCTTCCT | TTTTCAATAT  |
|      | ATTCCCGCTG  | TGCCTTTACA | ACTTATGAGT | ATGAGAAGCA | AAAGTTATA   |
| 2301 | TATTGAAGCA  | TTTATCAGGG | TTATTGTCTC | ATGAGCGGAT | ACATATTTGA  |
|      | ATAACTTCGT  | AAATACTCCC | ATAACAGAG  | TACTCGCCTA | TGTATAAACT  |
| 2351 | ATGTATTTAG  | AAAAATAAAC | AAATAGCCCT | TCCGCGCACA | TTTCCCCGAA  |
|      | TACATAAATC  | TTTTTATTTG | TTTATCCCCA | AGGCGCGTGT | AAAGGGCCTT  |
| 2401 | AAGTCCCACC  | TGACGTCTAA | GAAACCATTA | TTATCATGAC | ATTAACCTAT  |
|      | TTCACGCTGG  | ACTGCAGATT | CTTTGGTAAT | AATAGTACTG | TAATTGGATA  |
| 2451 | AAAATAGGC   | GTATCACCAG |            |            |             |
|      | TTTTTATCCG  | CATAGTGCTC |            |            |             |

FIGURE 7

pMOD (EEM-1)

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1  TCGCGCGTTT CCTGATGAC GGTCAAAACC TCTGACACAT GCAGCTCCCG
   AGCGCGCAA GCCACTACTG CCACPTTTGG AGACTGTGTA CGTGAGGGC
51  GAGACCGTCA CAGCTTGTCT GTAAGCGGAT GCCCGGAGCA GACAAACCCG
   CTCTGCCAGT GTGGAACAGA CATTCCGCTA CGGCCCTCGT CTGTTTGGCC
101 TCAGCGCGCG TCAGCGUETE TTGGCGGCTG TCGGAGCTGG CTTAACTATG
   AGTCCCGCGC AGTCCGCCAC AACCGCCAC AGCCCGGACC GAATTGATAC
                                     ApaLI
151 CGGCATCAGA GCAGATTGTA CTGAGGCTGC ACCATATGCG GTGTGAAATA
   CCGGTAGTCT CGTCTAACAT GACTCTCAGG TGGTATACCG CACACTTTAT
201 CCGCACAGAT GCGTAAGGAC AAAATACCGC ATCAGGCGCC ATTGCGCAT
   GCGGTGTCTA CGCATTCCTC TTTTATGGCG TAGTCCGCGG TAAGCGGTAA
251 CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC TCTTGGGTAT
   CTCGACGCGG TTGACAACCC TTCCCGCTAC CCACGCGCGG ACAAGCGATA
                                     EcoRI
301 TACGCCAGCT CTCTCTTATA CACATCTCAA CCATCATCGA TGAATTGAG
   ATCCGGTCGA CAGAGAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
                                     PvuII
351 CTCGGTACCG TACCATTCAA ATTTATCCTT ATTGTACAAA ATAACAGCGA
   CAGCCATGCC ATGGTAAGTT TAAATAGGAA TAACATGTTT TATTGTGCGT
                                     KpnI
401 AATTTTTTAA TCTATTCCTT ATCCATACAA ATTCCCGGTA GCGGCTAGGG
   TTAATAATTT AGATAAGGAA TAGCTATGTT TAAGGGGCGAT CCGCGATCC
451 ACCTCTTTAG CTCCTTGGA GCTGTGAGTA GTATACCTAA TAATTATCT
   TGGACAAATC GAGGAACCTT CGACAGTCAT CATATGGATT ATTAATAGA
501 ACATTCCCTT TACTAACGTG TAACCTTCCA AATTTACAAA AGCGACTCAT
   TGTAAAGGAA ATCATTGCAC ATTGAAGGTT TAAATGTTT TCGCTGAGTA
551 AGAATTATTT CCTCCGTTA AATAATAGAT AACTATTAAA ATAGACAAAT
   TCTTAATAAA GGAGGGCAAT TTATTATCTA TTGATAATTT TTATCTGTTA
601 ACTTGCTCAT AATTAACGGT ACTTAAATTG TTTACTTGG CGTGTTCAT
   TGAACGAGTA TTCATTGCCA TGAATTTAAC AATGAARCC GCACAAAGTA
651 TGCTTGAGAA ACTGATTTT AGTAACAGT TGAUGATATT CTCGATTGAC
   ACEAACACTT TGAATAAAA TCATTGTCA ACTGCTATAA GAGCTAACTG
701 CCATTTTGAA ACAAAGTACG TATATAGCTT CCAATATTTA TCTGGAACAT
   GGTAAAACTT TGTTCATGC ATATATCGAA GCTTATAAAT AGACCTTGT
751 CTGTGCTATG GCGGGTAAGT TTTATTAAGA CACTGTTTAC TTTTGGTTA
   GACACCATAC CGCCCATTC AATAATTTCT GTGACAAATG AAAACCAAT
801 CGATGAAAGC ATTCCGCTGG CAGCTTAAGC AATTGCTGAA TCGAGACTTG
   CCTACTTTTCG TAAGGCGACC GTCGAATTCG TTAACGACTT AGCTCTGAAC
851 AGTGTGCAAG AGCAACCTA GTGTCGGTG AATATCCAAG CTACGCTTGT
   TCACACGTTT TCGTTGGGAT CACAAGCCAC TTATAGGTTT CATGCGAACA
901 AGAATCCTTC TTCAACATC AGATAGATGT CAGACGCATG GCTTTCAAAA
   TCTTAGGAAG AAGTTGTTAG TCTATCTACA GTCTGCGTAC CGAAAGTTTT
951 ACCACTTTTT TAATAATTG TGTGCTTAAA TGGTAAGGAA TATCCCAAC
   TGGTGAAAAA ATTATTAAC ACACGAATTT ACCATTCTT ATAAGGGTTG
1001 AATTTTATAC CTCTGTTTGT TAGGGAAATG AACTGTAGA ATATCTTGGT
   TTAATAATATG GAGACAAACA ATCCCTTAAC TTTGACATCT TATAGAACCA

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pMOE (EX-1)

1051 GAAATTAAGT GACACGAATG ETCAGTCTTA ATTTTCTCGA CGATAACTTG  
 CTTAATTTCA CTGTCTTAC AAGTCAAAAT TAAAAAGSC GCTATTCAAC  
 1102 AATAGATGAC TGTCTAATTC AATAGACCTT ACCTGTTTAC TTATTTTAGC  
 TTATCTACTG ACAGATTAG TTATCTGCA TGGACAAATG AATAAAATCG  
 1151 CAGTTTCCTC GTTAAATGCU CTTTACCTGT TCCAATTTCT TAAACGGTAT  
 GTCAAAGCAG CAATTTACGG GAAATGGACA AGGTTAAAGC ATTTGCCATA  
 1201 CGGTTTCTTT TAAATTCAAT TGTTTTATTA TTTGGTTGAG TACCTTTTCA  
 GCCAAAGAAA ATTTAAGTAA ACAAATAAT AAACCAACTC ATGGAAGAGT  
 1251 TTCGTTAAAA AGTTTGGAGA ATATTTTATA TTTTGTTC TCTAATCACT  
 AAGCAATTTT TCAAACTCT TATAAATAT AAAACAAGT ACATTACTGA  
 1301 CCTGAAGTGA TACTCTATA AATAATACA GAAGTTAAAC GATTTGTTTG  
 CGACTTCACT ATGTAGATAT TTATTTATGT CTCAATTTG CTAACCAAAC  
 1351 TAATTTTAST TATCTGTTA AAAAGTCATA AGATTAGTCA CTGGTAGGAA  
 ATTAATTTCA ATAGACAAAT TTTTCAATAT TCTAATCAGT GACCATCCTT  
 1401 TTATCTTAAA CGTATTTATC TGCGTAATCA CTGTTTTTAC TCTGTTTCAA  
 AATTAGATTT GCATTAATAG ACGCAATAGT GACAAAAATC AGACAAAGTT  
 1451 AACAGTAGAT GTTTTATCTA CATTACGCAT TTGGATACC AACATGACGA  
 TTGTCATCTA CAAAATAGAT CTATGCGTA AACCTTATGG TTGTACTGCT  
 1501 ATCCCTCCTT CTTAATTACA AATTTTTAGC ATCTAATTTA ACTTCAATTC  
 TAGGGAGGAA GAATTAATGT TTAATAATCG TACATTAAAT TGAAGTTAAG  
 1551 CTATTATACA AAATTTTAAG ATAATGCACT ATCAACACAC TCTTAAGTTT  
 GATAATATGT TTTAAATTC TATTACCTGA TAGTTGTGTG AGAATTCAA  
 HindIII PvuII  
 1601 GCTTCTAAG CTTCAGGGTT GAGATGTCTA TAAGAGACAC CTGCATTAAT  
 CGAAGATTTT GAAGTCCCAA CTCTACACAT ATTCTCTGTC GAGGTAATTA  
 1651 GAATCGGCA ACGCGCGGGG AGAGGCGGT TCGTATTGG GCGCTCTCC  
 CTTACCGGT TCGGCGCGG TCTCGCCTAA ACGCATAACC CGCCAGAAGG  
 1701 GCTTCTCGC TCACTGACTC GCTCGGCTCG GTCGTTGCGG TCGGCGGAGC  
 CCAAGGAGCG AGTGAAGTGA CCACGCGAGC CAGCAAGCGG ACGCCGCTCG  
 1751 GGTATCAGCT CACTCAAAGG CGGTAAATCG GTTATCCACA GAATCAGGGG  
 CCATAGTCGA GTGAGTTTCC GCCATTATGC CAATAGGTGT CTTAGTCCCC  
 1801 ATAACGCAGG AAAGAACATG TGAGCAAAAG GCCAGCAAAA GGCCAGGAAC  
 TATTGCGTCC TTTCTGTGAC ACTCGTTTTC CGGTCGTTT CCGGTCCTTG  
 1851 CGTAAAAAGG CCGCGTTGCT GCGTTTTTTC CATAGGCTCC GCGCCCTTGA  
 GCATTTTTC GCGCAACGA CCGCAAAAG GTATCCGAGG GCGGGGGAAT  
 1901 CCAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG  
 GCTCGTAGTG TTTTAGCTG CGAGTTTCACT CTCCACCGCT TTGGGCTGTC  
 1951 GACTATAAAG ATACCAGGCG TTTCCCTCTG GAAGCTCCTT CGTGGCTCTT  
 CTGATATTTT TATGGTCCGC AAAGGGGGAC CTTCGAGGGA GCACGCGAGA  
 2001 CCTGTTCCGA CCTGCGGCT TACCGGATAC CTGTCCGCTT TTCTCCCTTC  
 GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGCGGGA AAGAGGGGAG  
 2051 GGGAGCGGTG GCGCTTTCTC ATAGCTCAUG CTGTAGGTAT CTCAGTTCGG  
 CCTTCCAC CCGGAAGAG TATCGAGTGC GACATCCATA GAGTCAAGCC  
 ApLI  
 2101 TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCGGTTCCAG  
 ACATCCAGCA ACGGAGGTTT GACCGGACAC ACGTGCTTGG GGGGCAAGTC  
 2151 CCGGACCGCT GCGCCTTATC CGGTAAGTAT CGTCTTGAAT CCAACCCGCT  
 GGGCTGCGGA CCGGAATAG GCCATTGATA GCAGAACTCA GGTGGGCA

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pMOD (Erm-1)

2201 AAGAACGGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA  
TTCTGTGCTG AATAGCGGTG ACCGTGCTCC CTGACCATTG TCCTAATCGT  
2251 GACCGAGGTA TGTAGGCGGT GTTACAGAGT TCTTGAAGTG GTGGCCTAAC  
CTCCCTCCAT ACATCCGCCA CCATGTCTCA AGAACCTTCA CACCGGATTG  
2301 TACGGCTACA CTAGAAGGAC AGTATTTGGT ATCTCCGCTC TGCTGAAGCC  
ATGCCGATGT GATCTTCCCTG TCATAAACCA TAGACGGGAG ACGACTTCGG  
2351 AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA  
TCAATGGAAAG CCTTTTCTCT AACCATCGAG AACTAGGCCG TTTGTTGGT  
2401 CUGCTGGTAG CGGTGGTTTT TTTGTTTCCA AGCAGCAGAT TACGCGCAGA  
GGUGAGCATC GCCACCAAA AAACAAAGCT TCGTCTCTA ATGCGGCTCT  
2451 AAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG GGTCTGACCC  
TTTTTTCTTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC CCAGACTGCC  
2501 TCAGTCCAAAC GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA  
AGTCACCTTG CTTTGAAGTG CAATTCCCTA AAACCAAGTAC TCTAATAGTT  
2551 AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG TTTTAAATCA  
TTTCCTAGAA GTGGATCTAG GAAAATTTAA TTTTACTTC AAAATTTAGT  
2601 ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAA  
TAGATTTCAT ATATACTCAT TTGAACCAGA CTGTCAATGG TTACCAATTA  
2651 CAGTGAGGCA CCTATCTCAG CGATCTCTCT ATTTCCGTTCA TCCATAGTTG  
GTCACTCCGT GGATACAGTC GCTAGACAGA TAAAGCAAGT AGGTATCAAC  
2701 CCTGACTCCU CGTCGTGTAG ATAACCTACG TACGGGAGGG CTTACCACT  
GGACTGAGGG GCAGCACATC TATTGATGCT ATGCCCTCCC GAATGGTACA  
2751 GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC CGGCTCCAGA  
CCGGGCTCAC GACGTTACTA TGGCGCTCTG GGTGCGAGTG CCGGAGGTCT  
2801 TTTATCAGCA ATAAACCAGC CACCCGGAAG GGCCGAGCGC AGAAGTGGTC  
AAATAGTCGT TATTGCTCG GTCCGCCCTC CCGGCTCGCG TCTTACCCAG  
2851 CTGGAATTT ATCCGCTTCC ATCCAGTCTA TTAATTGTTG CCGGGAAGCT  
GACGTTGAAA TAGGCGGAGG TAGGTGAGAT AATTAACAC CCGCCTTCGA  
2901 AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC  
TCTCATTCAT CAAGCGGTCA ATTATCAAAC GCGTTGCAAC AACGGTAACG  
2951 TACAGGCATC GTGGTGTAC GCTCGTCGTT TGGTATGGCT TCATTGAGCT  
ATGTCCGTAG CACCACAGTG CGAGCAGCAA ACCATACCGA AGTAAGTCGA  
3001 CCGGTTCCCA ACGATCAAGG CGAGTACAT GATCCCCCAT GTTGTGCAAA  
GGCCAAGGGT TGCTAGTTCC GCTCAATGTA CTAGGGGGTA CAACACGTTT  
3051 AAAGCGGTTA GTCCTTCGC TCCTCCGATC GTTGTGAGAA GTAGTTGGC  
TTTCGCCAAT CGAGGAAGCC AGGAGGCTAG CACAGTCTT CATTCACCCG  
3101 CGCAGTGTTA TCACTCATGG TTATGGCAGC ACTGCATAAT TCTCTTACTC  
GCGTCACAAT AGTGAGTACC AATACCGTGC TGACGTATTA AGAGAATGAC  
3151 TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA CTCAACCAAG  
AGTACGGTAG GCATTCTACG AAAAGACACT GACCACTCAT GAGTTGGTTC  
3201 TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC  
AGTAAGACTC TTATCACATA CGCCGCTGGC TCAACGAGAA CCGGCCGAG  
3251 AATACGGCAT AATACGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA  
TTATGCCCTA TTATGGCCG GTGTATCGTC TTGAATTTT CACGAGTAGT  
3301 TTGGAACACG TTCTTCGGGG CGAAACTCT CAAGGATCTT ACCGCTGTTG  
AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCCTAGAA TGGCGACAC

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PMOD (ZEM-1)

Apal I

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3351 AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAAGTGAT CTTCAGGATC
      TCTAGGTCAA GCTACATTGG GTGAGCACGT GGGTTGACTA GAAGTCGTAG
3401 TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA AGGCAAAATG
      AAAATCAAAG TGGTCGCAA GAGGCACTCG TTTTGTCTT TCGGTTTTAC
3451 CCGCAAAAAA GGGAAATAAG GCGACACGGA AATGTTGAT ACTCATACTC
      GGCCTTTTTT CCGTTATTCC CGCTGTCCCT TTACAACCTA TGAGTATCAG
3501 TTCCTTTTTT AATATTATTG AAGCATTTAT CAGGCTTATT GTCTCATGAC
      AAGGAAAAAG TTATAATAAC TTCTGTAAATA GTUCCAATAA CAGAGTACTC
3551 CCGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCCGC
      GCTATGTAT AACTTACAT AATCTTTTT ATTTCTTTAT CCCCAGGGCG
3601 GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAACAAAC CATTATTATC
      CGTGTAAAGG GGCTTTTCAC GGTGGACTGC AGATTCTTTG GTAATAATAG
3651 ATGACATTA CCTATAAAA TAGGGCTATC ACGAG
      TACTGTAATT GGATATTTTT ATCCGCATAG TGCTC
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pMOD (Cm)

FIGURE 8

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1  TCGCGGCTTT CCGTGATGAC GGTEAAAACC TGTGACACAT GCAGCTCCCG
   AGCGCGCAAA GCCACTACTC CCACTTTTUG AGACTGTETA CGTCGAGGGC
51  GAGACGOTCA CAGTTTGTCT GTAAGCGGAT GCCGGGAGCA GACAAGCCCG
   CTCTGCCAGT GTCGAACAGA CATTCCGCTA CGGCCCTCCT CTGTTCGGCC
101 TCAGGCGCGC TCACCGGGTG TTGCGGGGTG TCGGGGCTGG CTTAACTATE
   AGTCCGCGCG AGTCCCCCAC AACCGCCAC AGUCCGACC GAATTGATAC
                                     ApaLI
151 CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTGAAATA
   GCCGTAGTCT CGTCTAACAT GACTCTCAG TGGTATACGC CACACTTTAT
201 CCGCACAGAT CCGTAAGGAG AAAATACCGC ATCAGGCGCC ATTGCGCATT
   GCGGTGTCTA CCGATTCTTC TTTTATGGCG TAGTCCGCGG TAACCGGTAR
251 CAGGCTGCGC AACTGTGGG AAGGGCGATC GGTGCGGGCC TCTTCGCTAT
   GTCCGACGCG TTGACAACCC TTCCCGCTAG CCACGCGCGG AGAAGCGATA
                                     EcoRI
                                     ClaI
301 TACGCCAGCT GTCTCTTATA CACATCTCAA CCATCATCGA TGAATTGAG
   ATCGCGTCCA CAGAGAATAT GTGTAGAGTT GGTAGTAGCT ACTTAAGCTC
                                     PvuII
                                     KpnI
351 CTCGGTACCG TTAGTGACAT TAGAAAACCG ACTGTAAAA GTACAGTCCG
   GAGCCATGGC AATCACTGTA ATCTTTTGGC TGACATTTTT CATGTCACCC
401 CATTATCTCA TATTATAAAA GCCAGTCATT AGGCCTATCT GACAATTCCT
   GTAATAGAGT ATAATATTTT CGGTCACTAA TCCGGATAGA CTGTTAAGGA
451 GAATAGAGTT CATAACAAT CTTGCATCAT AACCATCACA AACACAATGA
   CTTATCTCAA GTATTGTTA GGACGTACTA TTGTAGTCT TTGTCTTACT
501 TGTACCTGTA AAGATAGCGG TAAATATATT GAATTACCTT TATTAAAGAA
   ACATGGACAT TTCTATCGCC ATTTATATAA CTTAATGGAA ATAATTACTT
551 TTTCCCTGCT GTAATAATGG GTAGAAGGTA ATTACTATTA TTATGATAT
   AAAAGGACGA CATTATTACC CATCTTCCAT TAATGATAAT AATAACTATA
                                     NcoI
601 TTAAGTTAAA CCCAGTAAAT GAAGTCCATG GAATAATAGA AAGAGAAAA
   AATTCAATTT GGGTCATTTA CTTCAGGTAC CTTATTATCT TTCTCTTTT
651 GCATTTTCAG GTATAGGTGT TTTGGGAAAC AATTTCCCGG AACCATTATA
   CGTAAAGTC CATATCCACA AAACCTTTG TTAAGGGGC TTGGTAATA
701 TTTCTCTACA TCAGAAAGGT ATATATCATA AAACCTTTG AAGTCATTCT
   AAAGAGATGT AGTCTTTCCA TATTTAGTAT TTGAGAAAC TTCAGTAAGA
751 TTACAGCAGT CCAATACCA GAGAATGTT TAGATACACC ATCAAAATTT
   AATGTCCTCA GGTATATGGT CTCTTACAAA ATCTATGTGG TAGTTTTTA
801 GTATAAAGTG GCTCTAAGT ATCCCAATAA CCTAAGTCTC CGTCGCTATT
   CATATTTTAC CGAGATTGAA TAGGGTTATT GGATTGAGAG GCAGCGATAA
851 GTAACCAGTT CTAAAAGCTG TATTTGAGTT TATCACCCTT GTCATAACA
   CATTGGTCAA GATTTTCGAC ATAACTCAA ATAGTGGGAA CAGTGATTC
901 AAATAAATGC AGGGTAAAT TTATATCCTT CTTGTTTTAT GTTTCGGTAT
   TTTATTTACG TCCCATTTA AATATAGGAA GAACAAAATA CAAAGCCATA
951 AAACACTAA TATCAATTTT TGTGGTTATA CTAAAAGTCG TTTGTTGGTT
   TTTTGTGATT ATAGTTAAG ACACCAATAT GATTTTCAGC AAACAACCAA
1001 CAAATAATGA TTAATATCT CTTTCTCTT CCAATTGCTT AATCAATTT
   GTTTATTACT AATTTATAGA GAAAGAGAA GGTAAACAGA TTTAGTTAAA

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|      |             |            |             |             |             |
|------|-------------|------------|-------------|-------------|-------------|
| 1051 | TATTAAAGTT  | CATTTGATAT | CCCTGCTAAA  | TTTTTATATA  | AAATGATTT   |
|      | ATAATTTCAA  | GTAACCTATA | CCGAGGATTT  | AAAAATAGAT  | TTCACTTAAA  |
| 1101 | AGGAGGCTTA  | CTTGCTGCT  | TTCTTCATTA  | CAATCAATCC  | TTTTTAAAA   |
|      | TGCTCGGAAT  | GAACAGAUGA | AAGAACTAAT  | CTTAGTTAGG  | AAAAAATTTT  |
|      |             | HindIII    |             |             | PvuII       |
| 1151 | GTCAATATTA  | CTGTAACAAG | CTTCAGGGTT  | GAGATGTGTA  | TAAGAGACAG  |
|      | CAGTTATAAT  | GACATTGTTC | GAAGTCCCAA  | CTCTACACAT  | ATTCTCTGTC  |
|      | PvuII       |            |             |             |             |
| 1201 | CTGCATTAAT  | GAATCGGCCA | ACGUGCGGGG  | AGAGGCCGTT  | TGCGTATTGG  |
|      | GACGTAATTA  | CTTAGCGGGT | TGUGUGGCCC  | TCTCCGCCAA  | ACGCATAACC  |
| 1251 | CGGCTCTTCC  | CCTTCCTCGC | TCACTGACTC  | GCTGCGCTCG  | GTGCTTCGGC  |
|      | CGCGAGAAAG  | CCAAGGAGCG | AGTGACTGAG  | CGACGGGAGC  | CAGCAAGCCG  |
| 1301 | TGCGGCGAGC  | GGTATCAGCT | CAC TCAAAGG | CGGTAATACG  | GTTATCCACA  |
|      | ACGCGGCTCG  | CCATACTCGA | GTGAGTTTCC  | GCCATTATGC  | CAATAAGTGT  |
| 1351 | GAATCAGGGG  | ATAACGCAGG | AAAGAACATG  | TGAGCAAAAG  | GCCACCAAAA  |
|      | CTTAGTCCCC  | TATTGCGTCC | TTTCTTGTAC  | AUTCCTTTTC  | CGGTCTTTTT  |
| 1401 | GGCCAGGAAC  | CGTAAATAAG | CCGCGTTGCT  | GGCGTTTTTC  | CATAGGCTCC  |
|      | CGGCTCCTTG  | GCATTTTTTC | GGCGCAACCA  | CGCAAAAAG   | GTATCCGAGG  |
| 1451 | GCCCCCCTGA  | CGAGCATCAC | AAAATCGAC   | GCTCAAGTCA  | GAGGTCCCGA  |
|      | CGGGCGGACT  | GCTCGTAGTG | TTTTTAGCTG  | CGAGTTCAGT  | CTCCACCCCT  |
| 1501 | AACCCGACAG  | GACTATAAAG | ATACCAGGCG  | TTTCCCCCTG  | GAAGCTCCCT  |
|      | TTGGGCTGTC  | CTGATATTTT | TATGGTCCGC  | AAAGGGGGAC  | CTTCGAGGGA  |
| 1551 | CGTGGCTCT   | CCTTTTCGGA | CCCTGCCGCT  | TACCGCATAC  | CTGTCCGCTT  |
|      | GCACGCGAGA  | GGACAAGGCT | GGGACCCCGA  | ATGGCCTATG  | GACAGGCGGA  |
| 1601 | TTCTCCCTTC  | GGGAAGCGTG | GCGCTTTCTC  | ATAGCTCAGC  | CTGTAGGTAT  |
|      | AAGAGGGAAC  | CCCTTCGCAC | CGCGAAAGAG  | TATCGAGTGC  | CACATCCATA  |
|      |             |            |             | ApalI       |             |
| 1651 | CTCAGTTCTG  | TGTAGGTCGT | TEGETGCAAG  | CTGGGCTGTG  | TGCACGAACC  |
|      | GAGTCAAGCC  | ACATCCAGCA | ACCGAGGTTT  | CACCCGACAC  | ACGTGCTTGG  |
| 1701 | CCGCGTTTCA  | CCCGACCGCT | GCGCCTTATC  | CGGTAACAT   | CGTCTTGACT  |
|      | GGGGCAAGTC  | GGGCTGGGGA | CGCGGAATAG  | GCCATTGATA  | GCAGAACTCA  |
| 1751 | CAAACCCGGT  | AAGACACGAC | TTATCGCCAC  | TGGCAGCAGC  | CAC TGGTAAC |
|      | GGTTGGGCCA  | TTCTGTGCTG | AATAGCGGTG  | ACCGTCGTCT  | GTGACCATTG  |
| 1801 | AGGATTAGCA  | GAGCGAGGTA | TGTAGGCGGT  | GCTACAGAGT  | TCTTGAAGTG  |
|      | TCCTAATCGT  | CTCGCTCCAT | ACATCCGCCA  | CGATGTCTCA  | AGAACTTCAC  |
| 1851 | GTGGCCTAAC  | TACCGCTACA | CTAGAAGGAC  | AGTATTTGGT  | ATCTGCGCTC  |
|      | CACCGCATTG  | ATGCCGATGT | GATCTTCTCT  | TCA TAAACCA | TAGACCGGAG  |
| 1901 | TGCTGAAGUC  | AGTTACCTTC | GGAAAAGAG   | TTGGTAGCTC  | TTGATCCGGC  |
|      | ACGACTTCTG  | TCAATGGAAG | CCTTTTCTCT  | AACCATCGAG  | AACTAGGCCG  |
| 1951 | AAACAAACCA  | CGGCTGGTAG | CGGTGGTTTT  | TTTGT TTGCA | AGCAGCAGAT  |
|      | TTTGT TTGCT | GGCGACCATC | GCCACCAAAA  | APACAAACGT  | TCGTGCTCTA  |
| 2001 | TACGCGCAGA  | AAAAAAGGAT | CTCAAGAAAG  | TCCTTTGATC  | TTTTCTACGG  |
|      | ATGCGCGTCT  | TTTTTTCCTA | GAGTTCTTCT  | AGGAAACTAG  | AAAAGATGCC  |
| 2051 | GGTCTGACGC  | TCAGTGGAAC | GAAAAC TCA  | GTTAAGGGAT  | TTTGGTCATG  |
|      | CCAGACTGUG  | AGTCACCTTG | CTTTTGAGTG  | CAATTCCCTA  | AAACCAGTAC  |
| 2101 | AGATTATCAA  | AAAGGATCTT | CACCTAGATC  | CTTTTAAATT  | AAAAATGAAG  |
|      | TCTAATAGTT  | TTTCCTAGAA | GTGGATCTAG  | GAAAATTTAA  | TTTTTACTTC  |

pMOD (Cm)

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2151 TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTCCTCT GACAGTTACC
    AAAATTTAGT TAGATTTTCAT ATATACTCAT TTGAACCAAG CTGTCAATTGG
2201 AATGCTTAAT CAGTGAGGCA CTTATCTCAG CGATCTGTCT ATTTCTTTCA
    TTACGAATTA GTCACTCGGT GCATAGAGTC GCTAGACAGA TAAAGCAAGT
2251 TCCATAGTTG CCTGACTCCC CCTCGTGTAG ATAACTACGA TACCGGAGGG
    AGGTATCAAC GGAAGAGGG GCACACATC TATTGATGCT ATGCCCTCCC
2301 CTTACCATCT GGCCCCAGTG CTGCAATGAT ACCGCCAGAC CCAGGCTCAC
    GAATGGTAGA CCGGGGTCAG GACGTTACTA TGGCGCTCTG GGTGCGAGTG
2351 CCGCTCCAGA TTTATCAGCA ATAAACCAAC CAGCCGGAAG GCGCGAGCGC
    GCGGAGGTCT AAATAGTCGT TATTTGGTCC CTCGGCCTTC CCGGCTCCCG
2401 AGAAGTGGTC CTGCAACTTT ATCCGCTCTC ATCCAGTCTA TTAATTCTTG
    TCTTCACCAAG GACGTTGAAA TAGGGCGGAGG TAGGTCAGAT AATTAAACAAC
2451 CCGGGAAGCT AGACTAAGTA GTTCCGCCAGT TAATAGTTTG CGCAACGTTG
    GGCCCTTCGA TCTCATTCAT CAAGCGCTCA ATTATCAAAC GCGTTCCAAC
2501 TTGCCATTGC TACAGGCATC GTCGTGTAC GCTCGTCGT TGGTATGGCT
    AACGGTAACG ATGTCCGTAG CACCACAGTG CGAGCAGCAA ACCATACCGA
2551 TCATTCAAGT CCGGTTCCCA ACGATCAAGG CGAGTTACAT GATCCCCCAT
    AGTAAGTCGA GGCCAAAGGT TGCTAGTTCC GCTCAATGTA CTAGGGGGTA
2601 GTTGTGCAAA AAGCGGGTTA GCTCCTTCGG TCCTCCGATC GTTGTGAGAA
    CAACACGTTT TTTCGCCAAT CGAGGAAGCC AGGAGGCTAC CAACAGTCTT
2651 GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCACC ACTGCATAAT
    CATTTCAACCG GCTTCACAAAT AGTGAGTACC AATACCGTCC TGACGTATTA
2701 TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA
    AGAGAATGAC AGTACGGTAG GCATTCTACG AAAAGACACT GACCACTCAT
2751 CTCAACCAAG TCATTCTGAC AATAGTGTAT GCGGCCACCG AGTTGCTCTT
    GAGTTGGTTC AGTAAGACTC TTATCACATA CGCCGCTGGC TCAACGAGAA
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2801 GGGGGGCGTC AATACGGGAT AATACCGGCG CACATAGCAG AACTTTAAAA
    CGGGCGCGCAG TTATGCCCTA TTATGCGGCG GTGTATCGTC TTGAAATTTT
2851 GTGCTCATCA TTGGAAAACG TTCCTCGGGG CGAAAACCTCT CAAGGATCTT
    CACGAGTAGT AACCTTTTGC AAGAAGCCCC GCTTTTGAGA GTTCTTAGAA
    ~~~~~~
 ApaLI
2901 ACCGCTGTTG AGATCCAGTT CGATGTAACC CACTCGTGCA CCCAACTGAT
 TGGCGACAAC TCTAGGTCAA GCTACATTTG GTGAGCACGT GGGTTGACTA
2951 CTTACGATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC AAAAACAGGA
 CAAGTCGTAG AAAATGAAAG TGGTCGCAAA GAUCCACTCG TTTTGTCTCT
3001 AGGCAAAATG CCGCAAAAAA GGGAAATACC GCGACACGGA AATGTTGAAT
 TCCGTTTTAC GCGGTTTTTT CCCTTATTCC CGCTGTGCCT TTACAACCTA
3051 ACTCATACTC TTCTTTTTTC AATATTATTG AAGCATTTAT CAGGGTTATT
 TGAGTATGAG AAGGAAAAAG TTATAATAAC TTCGTAAATA GTCCCAATAA
3101 GTCTCATGAG CGGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA
 CAGAGTACTC GCCTATGTAT AAACCTACAT AAATCTTTTT ATTTGTTTTAT
3151 GGGGTTCCGC GCACATTTCC CCGAAAAGTG CCACCTGACG TCTAACAAAC
 CCCCAGGGCG CGTGTAAAGG GGCTTTTTCAC GGTGGACTGC AGATTCTTTC
3201 CATTATTATC ATGACATTAA CCTATAAAAA TAGGCGTATC ACGAG
 GTAATAATAG TACTGTAATT GGATATTTTT ATCCGCATAG TGCTC

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